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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/623,611	10/06/2000	Gregory Coia	674537-2002	3929

20999 7590 06/27/2002

FROMMER LAWRENCE & HAUG  
745 FIFTH AVENUE- 10TH FL.  
NEW YORK, NY 10151

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JUL 29 2002  
TECH CENTER 1600/2900

EXAMINER

PONNALURI, PADMASHRI

ART UNIT PAPER NUMBER

1627

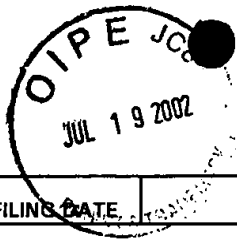
DATE MAILED: 06/27/2002

13

Please find below and/or attached an Office communication concerning this application or proceeding.

JUL - 1 A 10:20  
FROMMER, LAWRENCE  
& HAUG, LLP

DOCKETED



UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office  
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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/623,611	10/6/00		

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EXAMINER	
P. Ponnaluri	
ART UNIT	PAPER NUMBER
1627	13

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication filed on 4/26/02 is not fully responsive to the communication mailed 2/26/02. See the attached Raw Sequence Listing Error Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is given **ONE (1) MONTH or THIRTY (30) DAYS** from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

**PLEASE NOTE:** A reply to a notice to comply with the sequence rules should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office.

Please direct all replies to the United States Patent and Trademark Office via one (1) of the following:

1. Electronically submitted through EFS-Bio  
(<http://www.uspto.gov/ebs/efs/downloads/documents.htm>), EFS  
Submission User Manual - ePAVE)

2. Mailed to:  
U.S. Patent and Trademark Office  
Box Sequence, P.O. Box 2327  
Arlington, VA 22202

3. Mailed by Federal Express, United Parcel Service or other delivery  
service to:  
U. S. Patent and Trademark Office  
2011 South Clark Place  
Customer Window, Box Sequence  
Crystal Plaza Two, Lobby, Room 1B03  
Arlington, Virginia 22202



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**4. Hand Carried directly to the Customer Window at:  
2011 South Clark Place  
Crystal Plaza Two, Lobby, Room 1B03, Box Sequence,  
Arlington, Virginia 22202**

Any inquiry concerning this communication should be directed to P. Ponnaluri whose telephone number is (703) 305-3884. The examiner can normally be reached on Monday through Friday from 8:00 am to 4:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jyothsna Venkat, can be reached at (703)308-2439. The fax number for this group is (703)305-3014.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the group receptionist whose telephone number is (703)308-0196.

P. Ponnaluri  
Patent Examiner  
Technology center 1600  
Art Unit 1627  
25 June 2002

  
PADMASHRI PONNALURI  
PRIMARY EXAMINER

Application No.: 09/623,614

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

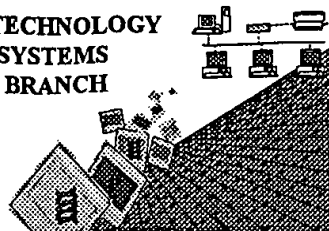
Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

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SYSTEMS  
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## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/623,611A  
Source: 1600  
Date Processed by STIC: 5/14/2002

#12  
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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

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VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
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<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/623,611A

DATE: 05/14/2002  
TIME: 15:50:03

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Output Set: N:\CRF3\05142002\I623611A.raw

3 <110> APPLICANT: Coia, et al.  
5 <120> TITLE OF INVENTION: V-like Domain Binding Molecules  
7 <130> FILE REFERENCE: 674537-2002  
9 <140> CURRENT APPLICATION NUMBER: 09/623,611A  
10 <141> CURRENT FILING DATE: 2000-10-06  
12 <150> PRIOR APPLICATION NUMBER: PCT/AU99/00136  
13 <151> PRIOR FILING DATE: 1999-03-05  
15 <150> PRIOR APPLICATION NUMBER: AU PP 2210  
16 <151> PRIOR FILING DATE: 1998-03-06  
18 <160> NUMBER OF SEQ ID NOS: 142  
20 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply  
Corrected Diskette Needed

*pp 1-2*

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#### ERRORED SEQUENCES

262 <210> SEQ ID NO: 18  
263 <211> LENGTH: 66  
264 <212> TYPE: DNA  
265 <213> ORGANISM: Artificial Sequence  
267 <220> FEATURE:  
268 <223> OTHER INFORMATION: oligonucleotide for CDR2 haemagglutinin tag  
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273 tgcacg  
609 <210> SEQ ID NO: 37  
610 <211> LENGTH: (67) 68 *shown*  
611 <212> TYPE: DNA  
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614 <220> FEATURE:  
615 <223> OTHER INFORMATION: oligonucleotide for CDR2 randomisation  
617 <220> FEATURE:  
618 <221> NAME/KEY: misc\_feature  
619 <222> LOCATION: (1)..(67)  
620 <223> OTHER INFORMATION: nucleotide 'n' can be any nucleotide 'a', 'c', 'g', or 't'.  
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624 <222> LOCATION: (1)..(67)  
625 <223> OTHER INFORMATION: 'k' is 'g' or 't'  
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E--> 631 ccatctg  
671 <210> SEQ ID NO: 40  
672 <211> LENGTH: (29) 30 (*see p. 2*)

(61) 60  
66

(60) 61  
(67) 68

## RAW SEQUENCE LISTING

DATE: 05/14/2002

PATENT APPLICATION: US/09/623,611A

TIME: 15:50:03

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673 &lt;212&gt; TYPE: DNA

674 &lt;213&gt; ORGANISM: Artificial Sequence

676 &lt;220&gt; FEATURE:

677 &lt;223&gt; OTHER INFORMATION: oligonucleotide for CDR2 randomisation

679 &lt;400&gt; SEQUENCE: 40

E--&gt; 680 gtagcatgccg cacagacttc agtcacctg

2372 &lt;210&gt; SEQ ID NO: 142

2373 &lt;211&gt; LENGTH: 6

E--&gt; 2374 &lt;212&gt; TYPE: Artificial Sequence

2375 &lt;213&gt; ORGANISM: CDR1 and CDR3 inserts possessing randomly generated sequence

2377 &lt;400&gt; SEQUENCE: 142

2379 SPECQD

2380 1

(29)30

*<212> this mandatory numeric identifier**<213> (should be)**and**if this is an amino acid sequence, response are missing**use three-letter amino acids,**and number the amino acids**under every 5 amino acids**insert <220>**(do not use TAB codes)**and <223> explanation goes on this line between amino acids)**FBI*

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 05/14/2002

PATENT APPLICATION: US/09/623,611A

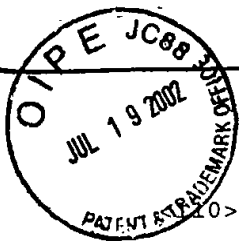
TIME: 15:50:04

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L:1706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97 after pos.:16  
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:0  
L:1728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:16  
L:1747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:0  
L:1766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:0  
L:1769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:16  
L:1788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:0  
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L:2374 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:





## SEQUENCE LISTING

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Coia, Gregory  
Galanis, Maria  
Hudson, Peter John  
Irving, Robert Alexander  
Nuttall, Stewart Douglas

<120> V-Like Binding Molecules

<130> 674537-2002

<140> 09/623,611

<141> 2000-10-06

<160> 142

<170> PatentIn version 3.1

<210> 1

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<212> PRT

<213> Homo Sapiens

<220>

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<223> conserved sequence in CDR3-like surface loop

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<211> 54

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<223> Oligonucleotide for CDR2 haemagglutinin tag

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<223> "s" can be g or c

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<223> "X" can be a,t,g or c

<220>  
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<222> (31)..(32)  
<223> "X" can be a,t,g or c

<220>  
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<222> (34)..(38)  
<223> "X" can be a,t,g or c

<220>  
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<222> (40)..(41)  
<223> "X" can be a,t,g or c

<220>  
<221> misc\_feature

<222> (43)..(44)  
<223> "X" can be a,t,g or c


<400> 32  
gccagctttg tgtgtgagta tgcannknnk nnknnknnkn nknnkggcgt ccgggtgaca 60  
gtgcttcggc agg 73

<210> 33  
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<220>  
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<220>  
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<223> "n" can be a,c,t or g

<220>  
<221> misc\_feature  
<222> (1)..(82)  
<223> "k" can be t or g

 <400> 33  
gccagctttg tgtgtgagta tgcannknnk nnknnknnkn nknnknnktg cnnkggcgtc 60  
cggggtgacag tgcttcggca gg 82

<210> 34  
<211> 82  
<212> DNA  
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<220>  
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<220>  
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<223> "n" can be a,t g or c

<220>  
<221> misc\_feature  
<222> (1)..(82)  
<223> "k" can be g or t

<400> 34

gccagctttg tgtgtgagta tgcannknnk ywynnkywyn nknnkywytg cnnkggcgtc 60  
cgggtgacag tgcttcggca gg 82

<210> 35  
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<220>  
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<223> "n" can be a,c,t or g

<220>  
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<223> "k" can be t or g

<220>  
<221> misc\_feature  
<222> (1)..(70)  
<223> "w" can be t or a

<220>  
<221> misc\_feature  
<222> (1)..(70)  
<223> "t" can be t or c

<220>  
<221> misc\_feature  
<222> (1)..(70)  
<223> "k" can be t or g

<400> 35  
gccagctttg tgtgtgagta tgcattctcca ggcnnknnkn nknnkgtccg ggtgacagtg 60  
cttcggcagg 70

<210> 36  
<211> 70  
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<220>  
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<223> "n" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (1)..(70)  
<223> "k" can be g or t

<400> 36  
gccagctttg tgtgtgagta tgcattctcca ggcnnktgcn nknkgtccg ggtgacagtg 60  
cttcggcagg 70

<210> 37  
<211> 68  
<212> DNA  
<213> Artificial Sequence

<220>  
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<220>  
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<223> "n" can be a,c,t or g

<220>  
<221> misc\_feature  
<222> (1)..(67)  
<223> "k" can be t or g

<400> 37  
gtgactgaag tctgtgcggc aacctacnnk nnkgggnnkg agttgacctt cctagatgat 60  
tccatctg 68

<210> 38  
<211> 30  
<212> DNA  
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<220>  
<223> Oligonucleotide for CDR-2 randomisation

<400> 38  
gtaggttgcc gcacagactt cagtcacctg 30

<210> 39

<211> 68  
<212> DNA  
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<220>  
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<223> "n" can be a,t,g or c

<220>  
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<222> (1)..(68)  
<223> "k" can be g or t

<400> 39  
gtgactgaag tctgtgcggc atgctacnnk nnkggggnkg agttgacctt cctagatgat 60  
tccatctg 68

<210> 40  
<211> 30  
<212> DNA  
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<220>  
<223> Oligonucleotide for CDR-2 randomisation

<400> 40  
gtagcatgcc gcacagactt cagtcacctg 30

<210> 41  
<211> 69  
<212> DNA  
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<220>  
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<222> (1)..(69)  
<223> "n" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (1)..(69)  
<223> "m" can be a or c

<400> 41  
ctgggtaccg ttgccgatgc cmnnmnnmnn mnnmnnmnnm nnnmnnmnnct ccaccttgca 60  
gatgtagag 69

<210> 42  
<211> 67  
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<220>  
<223> Oligonucleotide for CDR3 randomisation

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<223> "n" can be a,c,t or g

<220>  
<221> misc\_feature  
<222> (1)..(67)  
<223> "s" can be c or g

<400> 42  
aggtggaann snnsnnsnns nnsnnstgcn nsnnnsnnsn snnsnnsnns ggcacggca 60  
acggtac 67

<210> 43  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide for CDR3 randomisation

<220>  
<221> misc\_feature  
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<223> "n" can be a,t, g or c

<220>  
<221> misc\_feature  
<222> (1)..(78)  
<223> "m" can be a or c

<400> 43  
aatctgggta ccgttgccga tgccmnnmnn mnnmnnmnnm nnnmnnmnnm mnnncacctt 60  
gcagatgtag agtcccgt 78

<210> 44  
<211> 93  
<212> DNA  
<213> Artificial Sequence

<220>  
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<220>  
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<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (32)..(33)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (35)..(36)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (38)..(39)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (41)..(42)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (44)..(45)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (48)..(48)  
<223> "x" can be a,t,g or c

<220>  
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<222> (50)..(51)  
<223> "x" can be a,t,g or c

D/

<220>  
<221> misc\_feature  
<222> (53)..(54)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (56)..(57)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (59)..(60)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (62)..(63)  
<223> "x" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (65)..(66)  
<223> "x" can be a,t,g or c

① / <220>  
<221> misc\_feature  
<222> (47)..(47)  
<223> "x" can be a,t,g or c

<400> 44  
aatctgggta ccgttgccga tgcccagmnn mnnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60  
  
mnnmnnctcc accttcgaga tgtagagtcc cgt 93

<210> 45  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide for CDR3 randomisation

<220>  
<221> misc\_feature  
<222> (1)..(81)  
<223> "n" can be a,t,g or c

<220>



<221> misc\_feature  
<222> (1)..(81)  
<223> "m" can be a or c

<400> 45  
aatctgggta ccgttgccga tgccmnnmnn mnnmnnngcam nnnnnnnnnn nnnnnnnncac 60  
cttgcacgatg tagagtcccg t 81

<210> 46  
<211> 87  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide for CDR3 randomisation

<220>  
<221> misc\_feature  
<222> (1)..(87)  
<223> "n" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (1)..(87)  
<223> "m" can be a or c

<400> 46  
aatctgggta ccgttgccga tgccmnnmnn mnnmnnmnnng camnnnnnnnn nnnnnnnnnn 60  
mnnncaccttg cagatgtaga gtcccg t 87

<210> 47  
<211> 99  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide for CDR3 randomisation

<220>  
<221> misc\_feature  
<222> (1)..(99)  
<223> "n" can be a,c,t or g

<220>  
<221> misc\_feature  
<222> (1)..(99)  
<223> "m" can be a or c

<400> 47  
aatctgggta ccgttgccga tgccmnnmnn mnnmnnmnnm nngcamnnnn nnnnnnnnnn 60  
mnnmnnmnnm nnnnncacct tgcagatgta gagtcccg 99

<210> 48  
<211> 87  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide for CDR3 randomisation

<220>  
<221> misc\_feature  
<222> (1)..(87)  
<223> "n" can be a,t,g or c

<220>  
<221> misc\_feature  
<222> (1)..(87)  
<223> "m" can be a or c

<220>  
<221> misc\_feature  
<222> (1)..(87)  
<223> "r" can be a or g

<220>  
<221> misc\_feature  
<222> (1)..(87)  
<223> "w" can be a or t

<400> 48  
aatctgggta ccgttgccga tgccrwrnnn mnnmnnmnnng camnnnnnnn nnnnnnnnnn 60  
mnnncacctg cagatgtaga gtcccg 87

<210> 49  
<211> 70  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide for CTLA4 codon change

<400> 49  
atgcacgtgg cccagcctgc tgtggtgctg gccagcagcc gtggcatcgc cagctttgtg 60  
tgtgaatatg 70

<210> 50  
 <211> 77  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 50  
 gccagctttg tgtgtgaata tgcgtctggc tataccatcg gccgtactg catgggtgtg 60  
 cgtgtgaccg tgctgcg 77

<210> 51  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 51  
 gtgcgtgtga ccgtgctgcg tcaggcggat agccaggtga ccgaagtttg cgcg 54

<210> 52  
 <211> 75  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 52  
 caggtgaccg aagtttgcg ggcagcgatc aacatgggcg gtggcatcac cttcctggat 60  
 gattccatct gcacc 75

<210> 53  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 53  
 cagaccctgg atggtcaggt tcacctggtt accgctggag gtgccggtgc agatggaatc 60  
 atccag 66

<210> 54  
 <211> 57

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 54  
 cactttgcag atgtacagac cggtatccat ggcacgcaga ccctggatgg tcaggtt 57  
  
 <210> 55  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 55  
 caggccatga ccgcattcgt aataagacgc atagatggtg ctatccactt tgcagatgta 60  
 cagacc 66  
  
 <210> 56  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide for CTLA4 codon change  
  
 <400> 56  
 ctgggtaccg ttgccgatgc cagaatcgta gccatagcca ccggtggaca ggccatgacc 60  
 gcattcgta 69  
  
 <210> 57  
 <211> 672  
 <212> DNA  
 <213> Homo Sapiens  
  
 <220>  
 <221> CDS  
 <222> (109)..(453)  
 <223> Polynucleotide encoding Human CTLA-4 cDNA  
  
 <400> 57  
 atggcttgcc ttggatttca gcggcacaag gctcagctga acctggctgc caggacctgg 60  
 ccctgcactc tctgtttttt tcttctcttc atccctgtct tctgcaaa gca atg cac 117  
 Ala Met His  
 1  
 gtg gcc cag cct gct gtg gta ctg gcc agc agc cga ggc atc gcc agc 165

Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser  
5 10 15

ttt gtg tgt gag tat gca tct cca ggc aaa gcc act gag gtc cgg gtg 213  
Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val  
20 25 30 35

aca gtg ctt cgg cag gct gac agc cag gtg act gaa gtc tgt gcg gca 261  
Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala  
40 45 50

acc tac atg acg ggg aat gag ttg acc ttc cta gat gat tcc atc tgc 309  
Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys  
55 60 65

acg ggc acc tcc agt gga aat caa gtg aac ctc act atc caa gga ctg 357  
Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu  
70 75 80

agg gcc atg gac acg gga ctc tac atc tgc aag gtg gag ctc atg tac 405  
Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr  
85 90 95

cca ccg cca tac tac ctg ggc ata ggc aac gga acc cag att tat gta 453  
Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val  
100 105 110 115

attgatccag aaccgtgccc agattctgac ttctctctct ggatccttgc agcagttagt 513

tcgggggttgt ttttttatag ctttctctctc acagctgttt ctttgagcaa aatgctaaag 573

aaaagaagcc ctcttacaac aggggtctat gtgaaaatgc ccccaacaga gccagaatgt 633

gaaaagcaat ttcagcctta ttttattccc atcaattga 672

<210> 58  
<211> 115  
<212> PRT  
<213> Homo Sapiens

<400> 58

Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly  
1 5 10 15

Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu  
20 25 30

Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val  
35 40 45

Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp  
50 55 60

Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile  
65 70 75 80


Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu  
85 90 95

Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln  
100 105 110

Ile Tyr Val  
115

<210> 59  
<211> 7  
<212> PRT  
<213> Homo Sapiens

<400> 59

 Ser Pro Gly Lys Ala Thr Glu  
1 5

<210> 60  
<211> 14  
<212> PRT  
<213> Homo Sapiens

<400> 60

Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys  
1 5 10

<210> 61  
<211> 9  
<212> PRT  
<213> Homo Sapiens

<400> 61

Tyr Met Met Gly Asn Glu Leu Thr Phe  
1 5

<210> 62  
<211> 9  
<212> PRT  
<213> Homo Sapiens

<400> 62

Leu Met Tyr Pro Pro Pro Tyr Tyr Leu  
1 5

<210> 63  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Haemagglutinin tag

<400> 63

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

<210> 64  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Sequence from anti-lysozyme antibody

<400> 64

Ser Gly Tyr Thr Ile Gly Pro Tyr Cys Met Gly  
1 5 10

<210> 65  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Sequence from anti-lysozyme antibody

<400> 65

Thr Tyr Met Met Gly Asn Glu Leu Thr Phe  
1 5 10

<210> 66  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Sequence from anti-lysozyme antibody

<400> 66

Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu Cys Gly His Gly Leu Ser  
1 5 10 15

Thr Gly Gly Tyr Gly Tyr Asp Ser  
20

<210> 67  
<211> 11  
<212> PRT  
<213> Homo Sapiens

<400> 67

Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser  
1 5 10

<210> 68  
<211> 10  
<212> PRT  
<213> Homo Sapiens

<400> 68

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr  
1 5 10

<210> 69  
<211> 15  
<212> PRT  
<213> Homo Sapiens

<400> 69

Gly Trp Gly Leu Arg Gly Glu Glu Gly Asp Tyr Tyr Met Asp Val  
1 5 10 15

<210> 70  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Flag tag

<400> 70

Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Ala Asp Tyr Lys  
1 5 10 15

Asp Asp Asp Asp Lys  
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<210> 71  
<211> 14  
<212> PRT  
<213> Homo Sapiens

<400> 71

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu  
1 5 10

<210> 72  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> sequence from fusion protein

<400> 72

Ser Phe Val Cys Glu Tyr Ala Ser Gly Tyr Thr Ile Gly Pro Tyr Cys  
1 5 10 15

Met Gly

<210> 73  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> sequence from fusion protein

<400> 73

Ser Phe Val Cys Glu Tyr Ala Ala Gly Cys Lys Asn Phe Phe Trp Lys  
1 5 10 15

Thr Phe Thr Ser Cys Ala Thr Glu  
20

<210> 74  
<211> 18  
<212> PRT  
<213> Homo Sapiens

<400> 74

Ser Phe Val Cys Glu Tyr Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala


Met Ser

<210> 75  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> sequence from fusion protein containing the random sequence

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<222> (8)..(8)  
<223> "Xaa" can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> "Xaa" can be any amino acid

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<222> (10)..(10)  
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<220>  
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<222> (11)..(11)  
<223> "Xaa" can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (12)..(12)  
<223> "Xaa" can be any amino acid

<220>  
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<222> (13)..(13)  
<223> "Xaa" can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (14)..(14)  
<223> "Xaa" can be any amino acid

<400> 75

Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Gly  
1 5 10 15

<210> 76

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> sequence from fusion protein containing the random sequence

<220>

<221> MISC\_FEATURE

<222> (8)..(8)

<223> "Xaa" can be any amino acid

<220>

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<222> (9)..(9)

<223> "Xaa" can be any amino acid

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<222> (10)..(10)

<223> "Xaa" can be any amino acid

<220>

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<222> (11)..(11)

<223> "Xaa" can be any amino acid

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<222> (12)..(12)

<223> "Xaa" can be any amino acid

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<222> (13)..(13)

<223> "Xaa" can be any amino acid

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<223> "Xaa" can be any amino acid

<220>

<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> "Xaa" can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (17)..(17)  
<223> "Xaa" can be any amino acid

<400> 76

Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
1 5 10 15

Xaa Gly

<210> 77  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<222> (8)..(8)  
<223> "Xaa" can be any amino acid

<220>  
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<222> (9)..(9)  
<223> "Xaa" can be any amino acid

<220>  
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<222> (12)..(12)  
<223> "Xaa" can be any amino acid

<220>  
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<222> (15)..(15)  
<223> "Xaa" can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (16)..(16)  
<223> "Xaa" can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (20)..(20)  
<223> "Xaa" can be any amino acid

<400> 77

Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Ala Arg Xaa Ala Arg Xaa Xaa  
1 5 10 15

Ala Arg Cys Xaa Gly  
20

<210> 78  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<223> "Xaa" can be any amino acid

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<400> 79

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<210> 80  
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<400> 80

Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala  
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Thr Glu

<210> 81  
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<400> 81

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Thr Glu

<210> 82

<211> 24

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<400> 82

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Xaa Xaa Thr Ser Cys Ala Thr Glu  
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<210> 83  
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<400> 83

Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu  
1 5 10 15

Thr Phe Leu Asp Asp Ser Ile Cys Thr  
20 25

<210> 84  
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<400> 84

Gln Val Thr Glu Val Cys Ala Ala Ala Ile Asn Met Gly Gly Gly Ile  
1 5 10 15

Thr Phe Leu Asp Asp Ser Ile Cys Thr  
20 25

<210> 85  
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<400> 85

Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Pro Tyr Asp Val Pro Asp  
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Tyr Ala Leu Asp Asp Ser Ile Cys Thr  
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<400> 86

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Thr Tyr Leu Asp Asp Ser Ile Cys Thr  
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<210> 87  
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Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Xaa Xaa Gly Xaa Glu Leu  
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Thr Phe Leu Asp Asp Ser Ile Cys Thr  
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<210> 88  
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<400> 88

Gln Val Thr Glu Val Cys Ala Ala Cys Tyr Xaa Xaa Gly Xaa Glu Leu  
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Thr Phe Leu Asp Asp Ser Ile Cys Thr  
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<210> 89

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Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu  
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<210> 90

<211> 27

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<220>

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Cys Lys Val Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu Cys Gly His  
1 5 10 15

Gly Leu Ser Thr Gly Gly Tyr Gly Tyr Asp Ser  
20 25

<210> 91

<211> 18

<212> PRT

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<220>

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Cys Lys Val Glu Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr  
1 5 10 15

Ser Cys

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Cys	Lys	Val	Gly	Trp	Gly	Leu	Arg	Gly	Glu	Glu	Gly	Asp	Tyr	Tyr	Met
1				5					10					15	

Asp Val

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<400> 93

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<210> 94  
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<400> 94

Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
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Xaa Xaa

<210> 95  
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<400> 96

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1 5 10 15

<210> 97  
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1 5 10 15

Xaa

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<400> 98

Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa  
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<210> 99  
<211> 13  
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<400> 99

Cys Lys Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
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Cys Lys Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa

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Cys Lys Val Glu Ala Gly Cys Lys Asn Xaa Xaa Xaa Xaa Xaa Xaa Thr  
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Ser Cys

<210> 102  
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<400> 102

Leu Pro Ser Ser Asp Thr Arg Ala Tyr Ser  
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<210> 103  
<211> 8

<212> PRT  
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<220>  
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<400> 103

Gln Glu Ser Gly Gly Arg Pro Gly  
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<210> 104  
<211> 10  
<212> PRT  
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<220>  
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<400> 104

Leu Pro Arg Gly Pro Pro Leu Leu Ser Leu  
1 5 10

<210> 105  
<211> 7  
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<220>  
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<400> 105

Ser Pro Gly Arg Cys Leu Asn  
1 5

<210> 106  
<211> 8  
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<220>  
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<223> stop codon but Glu when expressed in Tg-1 or JM109 of E. col

<400> 106

Glu Trp Lys Arg Glu His Gly Gly

1

5

<210> 107  
<211> 10  
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<213> Artificial Sequence

<220>  
<223> CDR1 and CDR3 inserts possessing randomly generated sequence  
  
<400> 107

Leu Cys Pro Gly Ala Cys Gly Cys Val Tyr  
1 5 10

<210> 108  
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<220>  
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<223> stop codon but Glu when expressed in Tg-1 or JM109 strains of E.c  
ol

<400> 108

Asn Ser Gly Glu Asn Glu Gly Gly  
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<210> 109  
<211> 8  
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<400> 109

Asp Lys Pro Val Thr Lys Ser Gly  
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<210> 110  
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<222> (7)..(7)  
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ol

<400> 110

Ser Pro Gly Ala Cys Pro Glu  
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<210> 111  
<211> 7  
<212> PRT  
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<400> 111

Ser Pro Gly Lys Cys Asp Gln  
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21  
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<400> 112

Ser Pro Gly Met Cys Ala Arg  
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<400> 113

Pro Phe Leu Phe Leu Pro Cys Glu Phe Phe Phe  
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<210> 114

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR! and CDR3 inserts possessing randomly generated sequence

<400> 114

Trp Thr Leu Gly His His Lys Leu Cys Glu Gly  
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<210> 115

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 and CDR3 inserts possessing randomly generated sequence

<400> 115

Leu Phe Thr Cys Leu Leu Ala Leu Cys Ser  
1 5 10

<210> 116

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 and CDR3 inserts possessing randomly generated sequence

<400> 116

Ser Pro Gly Glu Cys Tyr Gly  
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<210> 117

<211> 13

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<220>

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<400> 117

Ser Trp Leu Ser Thr Thr Xaa Cys Leu Ser Ser Cys Ser  
1 5 10

<210> 118  
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<220>  
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<220>  
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ol

<400> 118

Ser Pro Gly Glu Cys Gln Asp  
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<210> 119  
<211> 13  
<212> PRT  
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<220>  
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<400> 119

Leu Leu Gly Ser Leu Leu Ser Cys Phe Ala Ser Leu Ser  
1 5 10

<210> 120  
<211> 13  
<212> PRT  
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<220>

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<400> 120

Ser Pro Gly Ser Leu Leu Ser Cys Phe Ala Ser Xaa Ser  
1 5 10

<210> 121  
<211> 7  
<212> PRT  
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<220>  
<223> CDR1 and CDR3 inserts possessing randomly generated sequence

<400> 121

Ser Pro Gly Arg Cys Thr Asp  
1 5

<210> 122  
<211> 13  
<212> PRT  
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<400> 122

Val Ile Cys His Ser Ser Val Cys Leu Ser Asp Val Cys  
1 5 10

<210> 123  
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<220>  
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<400> 123

Val Ile Cys His Ser Ser Val Cys Leu Ser Glu Val Cys  
1 5 10

<210> 124  
<211> 10  
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<220>  
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<400> 124

Asp Leu Pro Ser Tyr Leu Ala Cys Ser Ile  
1 5 10

<210> 125  
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<220>  
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<400> 125

Ser Pro Gly Arg Cys Asp Ala  
1 5

<210> 126  
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<220>  
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<400> 126

Ala Leu Cys Trp Asp Val Phe Tyr Cys Ser Phe Pro Ser Tyr  
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<210> 127  
<211> 11  
<212> PRT  
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<400> 127

Glu Leu Phe Gly His Ala Arg Tyr Cys Lys Gly  
1 5 10

<210> 128  
<211> 15  
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Val Ser Ile Thr Ser Pro Glu Leu Cys Pro Val Lys Val Phe Asp  
1 5 10 15

<210> 129  
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<212> PRT  
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<220>  
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<400> 129

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1 5

<210> 130  
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Leu Phe Val Pro Phe Val Ser Pro  
1 5

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Ser Pro Gly Asp Leu Trp Val  
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Glu Ser Gly Leu Ser Pro Val Ser Pro Cys Ser Leu Tyr Ser Leu  
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<210> 133

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Thr Ser Ala Asn Gly Pro Tyr Gly  
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<210> 135

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Phe Trp Lys Thr  
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<213> Homo Sapiens

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Gly Phe Cys Cys Cys  
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Ser Pro Glu Cys Gln Asp  
1 5

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Creation date: 02-03-2004  
Indexing Officer: HLE11 - LE HUNG  
Team: OIPEBackFileIndexing  
Dossier: 09623611

Legal Date: 08-13-2002

No.	Doccode	Number of pages
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Total number of pages: 5

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